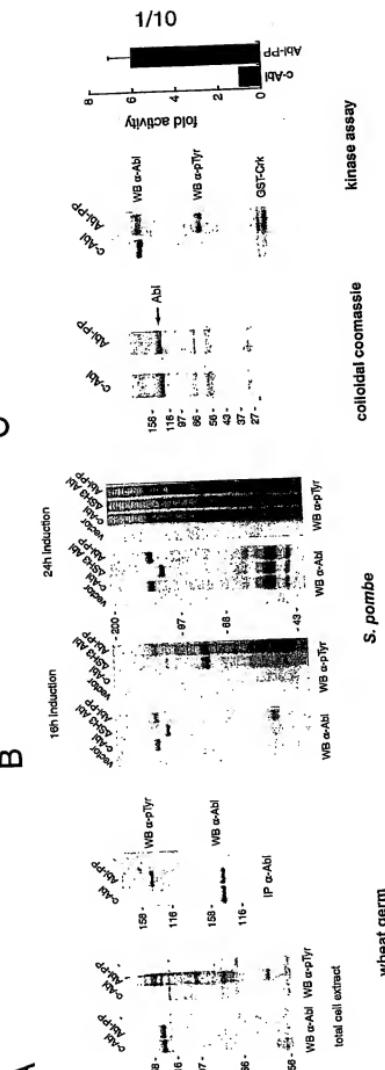


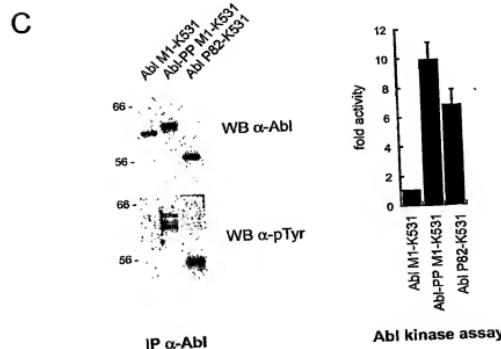
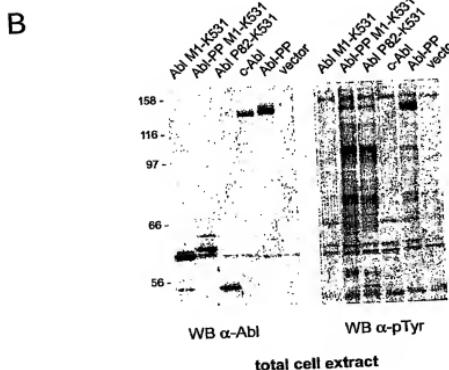
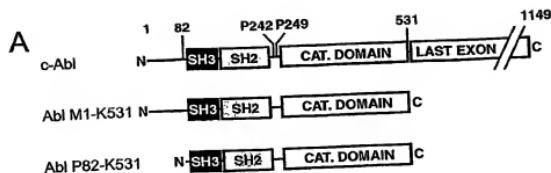
FIG. 1



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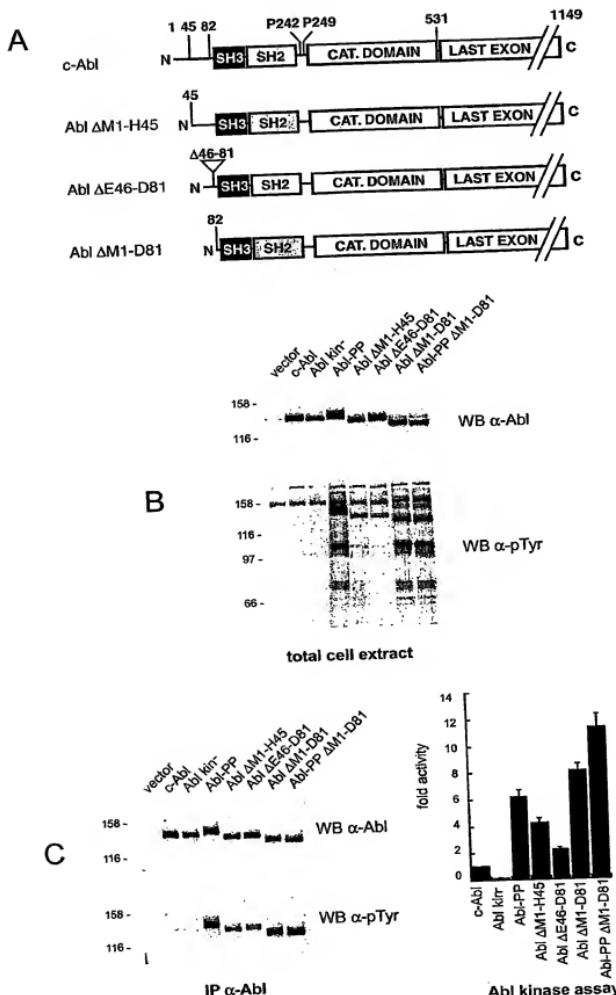
2/10

FIG. 2



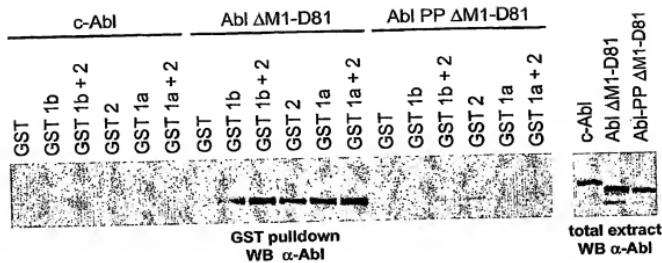
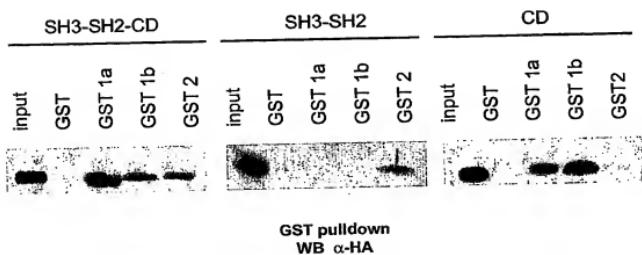
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FIG. 3



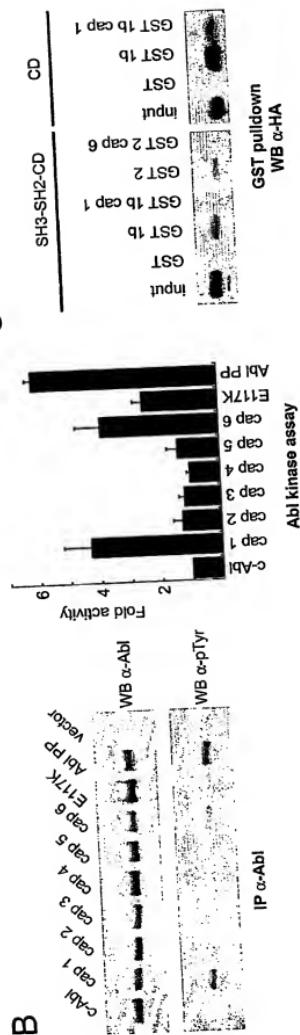
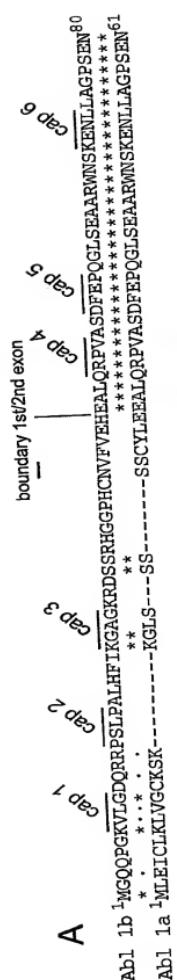
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FIG. 4

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5/10

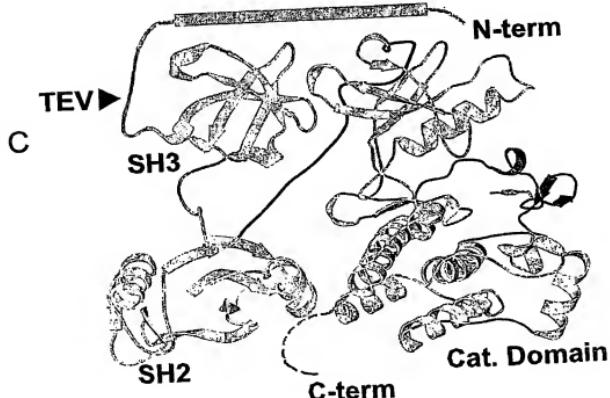
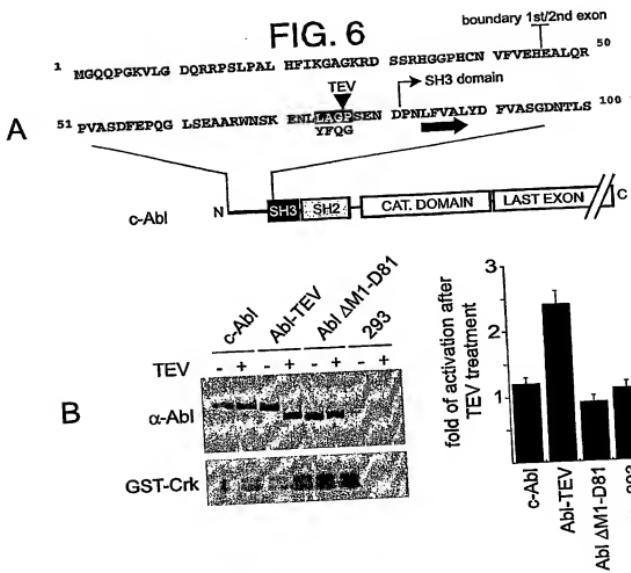
FIG. 5



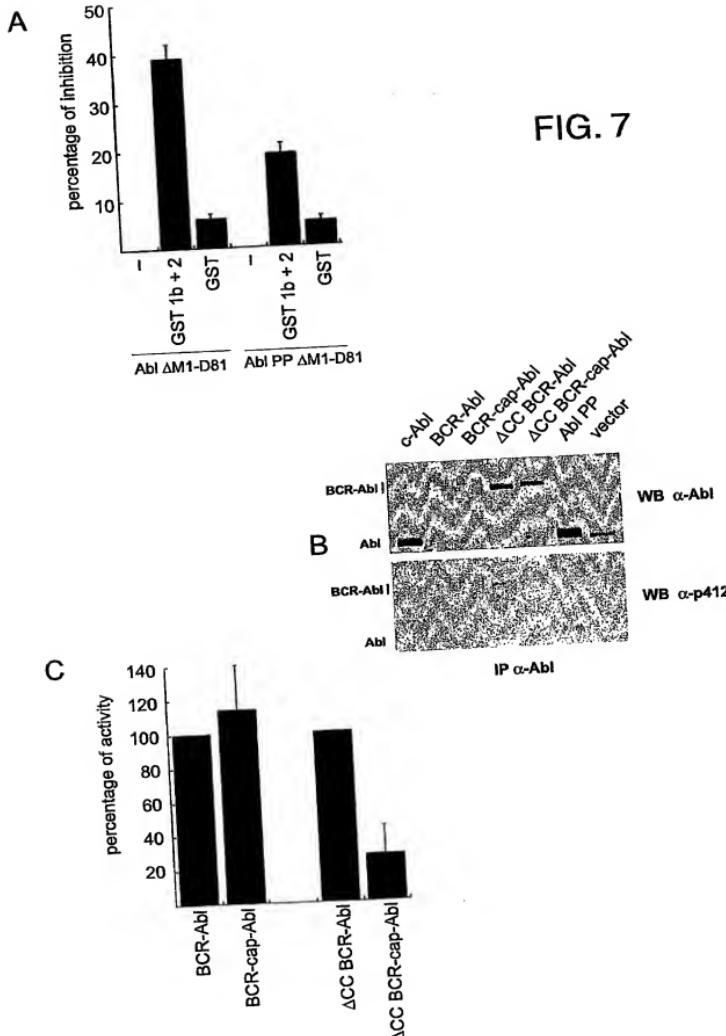
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6/10

FIG. 6



7/10



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8/10

FIG 8

hAb1la	MLEICLKL-----VGCKSK-----KGLSSSSS-----C-YLEE-
mAb1I	MLEICLKL-----VGCKSK-----KGLSSSSS-----C-YLEEH
hAb1lb	MGQQPGKV----- LGDQRRPSLPA LHFIKGAGKRDSSRHGGP-----HCNVFVEH
mAb1IV	MGQQPGKV----- LGDQRRPSLPA LHFIKGAGKRDSSRHGGP-----HCNVFVEH
hArg1a	--MVLGTV----LLPPN-----TYGRDQDTS-----LCCLCTEA
hArg1b	MGQQVGRVGEAPGLQQPQRGIRGSSAARPSGRRRDPAGRITETGFNIFTQHDHFASCVED
hAb1la	-----AIQRPVASDFEPQGLSEARWNS <u>KEN</u> LLAGPSEN----- 61
mAb1I	-----EALQRPVASDFEPQGLSEARWNS <u>KEN</u> LLAGPSEN----- 63
hAb1lb	-----EALQRPVASDFEPQGLSEARWNS <u>KEN</u> LLAGPSEN----- 92
mAb1IV	-----EALQRPVASDFEPQGLSEARWNS <u>KEN</u> LLAGPSEN----- 80
hArg1a	---SESALPDLTEALHRPYGCDEVQALNEAIRWSS <u>KEN</u> LLGATES----- 71
hArg1b	GFE GDKTGGSSPEALHRPYGCDEVQALNEAIRWSS <u>KEN</u> LLGATES----- 107

Legend:

Bold: cap 1 domain

Underlined: cap 6 domain

Bold italic: conserved domain upstream of cap 6 domain that forms an alpha helix with cap 6 domain

9/10

FIG 9

hAb1la	-----	-----
mAb1I	-----	-----
hAb1lb	-----	-----
mAb1IV	-----	-----
hArg	ATGGGGCAGCAGGTGGGCCGCGTCGGGAAGCTCCGGGCTCCAGCAGCCTAGCCCCGC	60
hAb1la	-----	-----
mAb1I	-----	-----
hAb1lb	-----	ATGGGGCAGCAGCCTGGAAAAGTCTTGGGGACCAAAG 38
mAb1IV	-----	ATGGGGCAGCAGCCTGGAAAAGTCTTGGGGACCAAAG 38
hArg	GGGATCCGGGGCAGCAGTGCAGGCCAGGCCCTCCGGCGCAGGCCGGACCCGGCGGGCGC	120
hAb1la	-----	ATGTTGGAGATCTGCCCTGAAGCTGGTGGGCTGCAAATCCAAGAAGG 46
mAb1I	-----	ATGTTGGAGATCTGTTGAAGTGGTGGGCTGCAAATCCAAGAAGG 46
hAb1lb	AAGGCCTAGTTGCCCGCCCTGCATTTATCAAAGGGCAGGGAAAGAGGGACTCATCGAG	98
mAb1IV	AAGGCCTAGTTGCCCGCCCTGCATTTATCAAAGGGCAGGGAAAGAGGGACTCATCGAG	98
hArg	ACCACAGAGACCGGTTCAATATCTCACCCAGCATGATCACTTGCCAG-CTGTGTGGA	179
hAb1la	GGCTGTCTCGTCCTCCAGCTGTATCTGGAGAA-----	98
mAb1I	GGCTCTCTCGTCCTCCAGCTGCTACCTGGAGGAACAC--GAAGCCCTGCAGAGGCCAGT	104
hAb1lb	GCATGGGGC-CCACACTGCAATGCTTGTGGAACAC--GAGCCCTGCAGAGGCCAGT	155
mAb1IV	GCATGGGGC-CCACACTGCAATGCTTGTGGAACAC--GAAGCCCTGCAGAGGCCAGT	155
hArg	GGATGGATTGAGGGAGACAAGACTGGAGGCAGTAGTCCAGAAGCTTGCATCGCCCTA	239

10/10

hAb1la GGCATCTGACTTTGAGCCCCAGGGTCTCAGCGAAAGCAGCTCGATGGAACCTCCAAGGAAAA 158
mAb1I GGCATCTGACTTTGAGCCCCAGGGTCTCAGCGAAAGCAGCTCGATGGAACCTCCAAGGAAAA 164
hAb1lb GGCATCTGACTTTGAGCCCCAGGGTCTCAGCGAAAGCAGCTCGATGGAACCTCCAAGGAAAA 215
mAb1IV GGCATCTGACTTTGAGCCCCAGGGTCTCAGCGAAAGCAGCTCGATGGAACCTCCAAGGAAAA 215
hArg TGGTTGTGATGTTGAACCCCAGGGACTAAATGAGGCTATCAGGTGGAGCTCCAAGGAGAA 299

hAb1la CCTTCTTGCTGGGCCAGTGAAAAT----- 183
mAb1I CCTTCTTGCTGGGCCAGTGAAAAT----- 189
hAb1lb CCTTCTTGCTGGGCCAGTGAAAATGACCCCAACCTTTGTGGACTCTATGATTGT 275
mAb1IV CCTTCTTGCTGGGCCAGTGAAAAT----- 240
hArg CTTGCTCG---GAGCCACTGAGAGTGACCCCTAAT----- 330

hAb1la -

mAb1I -

hAb1lb G 276

mAb1IV -

hArg -